










































Related Structures

Sequences producing significant alignments:			Score	E	
			(bits)	Value	
<a href="#">gi 6912284 ref NP_036245.1 </a>	<a href="#">carbonic anhydrase XIV precursor...</a>	<a href="#">682</a>	0.0	<a href="#">L</a>	
<a href="#">gi 22760422 dbj BAC11191.1 </a>	<a href="#">unnamed protein product [Homo s...</a>	<a href="#">681</a>	0.0	<a href="#">L</a>	
<a href="#">gi 6753264 ref NP_035927.1 </a>	<a href="#">carbonic anhydrase 14; CA XIV [...</a>	<a href="#">548</a>	e-155	<a href="#">L</a>	
<a href="#">gi 47168790 pdb 1R35 A</a>	<a href="#">Chain A, Crystal Structure of The Ex...</a>	<a href="#">438</a>	e-122	<a href="#">S</a>	
<a href="#">gi 21431756 sp Q9MZ30 CAHC_RABIT</a>	<a href="#">Carbonic anhydrase XII pre...</a>	<a href="#">270</a>	3e-71		
<a href="#">gi 4502515 ref NP_001209.1 </a>	<a href="#">carbonic anhydrase XII isoform ...</a>	<a href="#">264</a>	2e-69	<a href="#">L</a>	
<a href="#">gi 30585185 gb AAP36865.1 </a>	<a href="#">Homo sapiens carbonic anhydrase ...</a>	<a href="#">263</a>	5e-69		
<a href="#">gi 45935383 ref NP_996808.1 </a>	<a href="#">carbonic anhydrase XII isoform...</a>	<a href="#">263</a>	5e-69	<a href="#">L</a>	
<a href="#">gi 26342835 dbj BAC35074.1 </a>	<a href="#">unnamed protein product [Mus mu...</a>	<a href="#">262</a>	9e-69	<a href="#">L</a>	
<a href="#">gi 31541884 ref NP_848483.2 </a>	<a href="#">carbonic anyhydrase 12 [Mus mu...</a>	<a href="#">261</a>	1e-68	<a href="#">L</a>	
<a href="#">gi 34864283 ref XP_343417.1 </a>	<a href="#">similar to 2310047E01Rik prote...</a>	<a href="#">261</a>	1e-68	<a href="#">L</a>	
<a href="#">gi 47221597 emb CAF97862.1 </a>	<a href="#">unnamed protein product [Tetrao...</a>	<a href="#">261</a>	2e-68		
<a href="#">gi 21595173 gb AAH31385.1 </a>	<a href="#">Car12 protein [Mus musculus]</a>	<a href="#">260</a>	3e-68	<a href="#">L</a>	
<a href="#">gi 47225853 emb CAF98333.1 </a>	<a href="#">unnamed protein product [Tetrao...</a>	<a href="#">254</a>	1e-66		
<a href="#">gi 34858063 ref XP_342298.1 </a>	<a href="#">similar to CA XIV [Rattus norv...</a>	<a href="#">246</a>	4e-64	<a href="#">L</a>	
<a href="#">gi 15826782 pdb 1JCZ A</a>	<a href="#">Chain A, Crystal Structure of The Ex...</a>	<a href="#">246</a>	6e-64	<a href="#">S</a>	
<a href="#">gi 47211349 emb CAF93821.1 </a>	<a href="#">unnamed protein product [Tetrao...</a>	<a href="#">240</a>	3e-62		
<a href="#">gi 47228789 emb CAG07521.1 </a>	<a href="#">unnamed protein product [Tetrao...</a>	<a href="#">236</a>	4e-61		
<a href="#">gi 49117984 gb AAH72918.1 </a>	<a href="#">Unknown (protein for MGC:80389) ...</a>	<a href="#">209</a>	5e-53		
<a href="#">gi 9955948 ref NP_001207.1 </a>	<a href="#">carbonic anhydrase IX precursor...</a>	<a href="#">203</a>	4e-51	<a href="#">L</a>	
<a href="#">gi 21314850 ref NP_647466.1 </a>	<a href="#">carbonic anhydrase 9 [Mus musc...</a>	<a href="#">201</a>	2e-50	<a href="#">L</a>	
<a href="#">gi 30580354 sp Q8VHB5 CAH9_MOUSE</a>	<a href="#">Carbonic anhydrase IX prec...</a>	<a href="#">201</a>	2e-50	<a href="#">L</a>	
<a href="#">gi 115469 sp P08060 CAH6_SHEEP</a>	<a href="#">Carbonic anhydrase VI (Carbo...</a>	<a href="#">197</a>	2e-49		
<a href="#">gi 89853 pir A29993</a>	<a href="#">carbonate dehydratase (EC 4.2.1.1) VI ...</a>	<a href="#">197</a>	4e-49		
<a href="#">gi 34935135 ref XP_233380.2 </a>	<a href="#">similar to carbonic anhydrase ...</a>	<a href="#">196</a>	5e-49	<a href="#">L</a>	
<a href="#">gi 27806915 ref NP_776323.1 </a>	<a href="#">carbonic anhydrase VI [Bos tau...</a>	<a href="#">195</a>	1e-48	<a href="#">L</a>	
<a href="#">gi 28812184 dbj BAC65098.1 </a>	<a href="#">carbonic anhydrase VI [Canis fa...</a>	<a href="#">189</a>	6e-47	<a href="#">L</a>	
<a href="#">gi 14530767 emb CAC42429.1 </a>	<a href="#">dJ477M7.5 (carbonic anhydrase V...</a>	<a href="#">186</a>	5e-46	<a href="#">L</a>	
<a href="#">gi 1070519 pir CRHU6</a>	<a href="#">carbonate dehydratase (EC 4.2.1.1) VI...</a>	<a href="#">184</a>	3e-45		
<a href="#">gi 23503046 sp P23280 CAH6_HUMAN</a>	<a href="#">Carbonic anhydrase VI prec...</a>	<a href="#">181</a>	1e-44	<a href="#">L</a>	
<a href="#">gi 4557397 ref NP_001206.1 </a>	<a href="#">carbonic anhydrase VI precursor...</a>	<a href="#">181</a>	2e-44	<a href="#">L</a>	
<a href="#">gi 31076619 sp Q8UWA5 CAH2_TRIHK</a>	<a href="#">Carbonic anhydrase II (Car...</a>	<a href="#">180</a>	5e-44		
<a href="#">gi 34872490 ref XP_216584.2 </a>	<a href="#">similar to Car6 protein [Rattu...</a>	<a href="#">179</a>	7e-44	<a href="#">L</a>	
<a href="#">gi 40363537 ref NP_954685.1 </a>	<a href="#">carbonic anhydrase II [Danio r...</a>	<a href="#">177</a>	3e-43	<a href="#">L</a>	
<a href="#">gi 29789369 ref NP_599183.1 </a>	<a href="#">protein tyrosine phosphatase, ...</a>	<a href="#">176</a>	6e-43	<a href="#">L</a>	
<a href="#">gi 25281969 gb AAN72430.1 </a>	<a href="#">receptor-like protein tyrosine p...</a>	<a href="#">176</a>	6e-43	<a href="#">L</a>	
<a href="#">gi 6679559 ref NP_033007.1 </a>	<a href="#">protein tyrosine phosphatase, r...</a>	<a href="#">176</a>	7e-43	<a href="#">L</a>	
<a href="#">gi 25281971 gb AAN72431.1 </a>	<a href="#">receptor-like protein tyrosine p...</a>	<a href="#">176</a>	1e-42	<a href="#">L</a>	
<a href="#">gi 45709528 gb AAH67635.1 </a>	<a href="#">LOC407683 protein [Danio rerio]</a>	<a href="#">174</a>	2e-42	<a href="#">L</a>	
<a href="#">gi 45383516 ref NP_989645.1 </a>	<a href="#">protein tyrosine phosphatase, ...</a>	<a href="#">174</a>	2e-42	<a href="#">L</a>	
<a href="#">gi 18860898 ref NP_002832.2 </a>	<a href="#">protein tyrosine phosphatase, ...</a>	<a href="#">174</a>	3e-42	<a href="#">L</a>	
<a href="#">gi 1263069 gb AAC50439.1 </a>	<a href="#">receptor tyrosine phosphatase gam...</a>	<a href="#">174</a>	3e-42	<a href="#">L</a>	
<a href="#">gi 477137 pir A48148</a>	<a href="#">protein-tyrosine-phosphatase (EC 3.1....</a>	<a href="#">173</a>	5e-42		
<a href="#">gi 25281973 gb AAN72432.1 </a>	<a href="#">receptor-like protein tyrosine p...</a>	<a href="#">172</a>	7e-42	<a href="#">L</a>	
<a href="#">gi 41387130 ref NP_957107.1 </a>	<a href="#">hypothetical protein MGC73385 ...</a>	<a href="#">172</a>	1e-41	<a href="#">L</a>	
<a href="#">gi 29179452 gb AAH49309.1 </a>	<a href="#">Zgc:73385 protein [Danio rerio]</a>	<a href="#">169</a>	1e-40	<a href="#">L</a>	
<a href="#">gi 5921196 sp P18761 CAH6_MOUSE</a>	<a href="#">Carbonic anhydrase VI precu...</a>	<a href="#">168</a>	1e-40	<a href="#">L</a>	
<a href="#">gi 33585712 gb AAH55437.1 </a>	<a href="#">Car6 protein [Mus musculus]</a>	<a href="#">166</a>	9e-40	<a href="#">L</a>	
<a href="#">gi 29612611 gb AAH49973.1 </a>	<a href="#">Car6 protein [Mus musculus]</a>	<a href="#">166</a>	9e-40	<a href="#">L</a>	
<a href="#">gi 50418465 gb AAH78387.1 </a>	<a href="#">Unknown (protein for IMAGE:70369...</a>	<a href="#">164</a>	3e-39		
<a href="#">gi 34851195 ref XP_226204.2 </a>	<a href="#">similar to carbonic anhydrase ...</a>	<a href="#">161</a>	2e-38	<a href="#">L</a>	
<a href="#">gi 68286 pir CRRB2</a>	<a href="#">carbonate dehydratase (EC 4.2.1.1) II -...</a>	<a href="#">161</a>	2e-38		

gi 2098445 pdb 1UGF	Human Carbonic Anhydrase Ii [hcai] (...)	161	3e-38	
gi 28269695 ref NP_444300.1	carbonic anhydrase 7; carbonic...	160	4e-38	
gi 47227809 emb CAG08972.1	unnamed protein product [Tetrao...	159	7e-38	
gi 4557395 ref NP_000058.1	carbonic anhydrase II; carbonat...	159	7e-38	
gi 1942501 pdb 1UGD	Human Carbonic Anhydrase Ii[hcai] (E...	159	7e-38	
gi 2118910 pir A48993	protein-tyrosine-phosphatase (EC 3.1...	159	9e-38	
gi 11513906 pdb 1G3Z A	Chain A, Carbonic Anhydrase Ii (F131...	159	1e-37	
gi 15080386 gb AAH11949.1	Carbonic anhydrase II [Homo sapi...	159	1e-37	
gi 229731 pdb 1CA2	Carbonic Anhydrase II (Carbonate Dehyd...	159	1e-37	
gi 442669 pdb 1BCD	Carbonic Anhydrase Ii (E.C.4.2.1.1) Co...	159	1e-37	
gi 1421269 pdb 1CAN	Carbonic Anhydrase Ii (E.C.4.2.1.1) C...	159	1e-37	
gi 1942500 pdb 1UGB	Human Carbonic Anhydrase Ii[hcai] (E...	159	1e-37	
gi 38348436 ref NP_940986.1	carbonic anhydrase XIII; carbo...	159	1e-37	
gi 1942499 pdb 1UGA	Human Carbonic Anhydrase Ii[hcai] (E...	159	1e-37	
gi 2098448 pdb 1UGE	Human Carbonic Anhydrase Ii [hcai] (...)	159	1e-37	
gi 115448 sp P00917 CAH1_HORSE	Carbonic anhydrase I (Carbon...	158	1e-37	
gi 22219225 pdb 1LG5 A	Chain A, Crystal Structure Analysis ...	158	1e-37	
gi 2098447 pdb 1UGC	Human Carbonic Anhydrase Ii [hcai] (...)	158	2e-37	
gi 22252956 gb AAM94169.1	erythrocyte carbonic anhydrase [...]	158	2e-37	
gi 68288 pir CRBO2	carbonate dehydratase (EC 4.2.1.1) II -...	158	2e-37	
gi 442701 pdb 1CAJ	Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu...	158	2e-37	
gi 1065006 pdb 1CNH	Carbonic Anhydrase Ii (Carbonate Dehy...	158	2e-37	
gi 999629 pdb 1YDB	Carbonic Anhydrase Ii (Carbonate Dehyd...	158	2e-37	
gi 231119 pdb 5CA2	Carbonic Anhydrase II (Carbonate Dehyd...	157	2e-37	
gi 1633065 pdb 1ZSC	Carbonic Anhydrase Ii Mutant E117q, H...	157	3e-37	
gi 442702 pdb 1CAK	Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu...	157	3e-37	
gi 46048696 ref NP_990648.1	carbonic anhydrase II [Gallus ...]	157	3e-37	
gi 231199 pdb 6CA2	Carbonic Anhydrase II (Carbonate Dehyd...	157	3e-37	
gi 442772 pdb 1CVA	Carbonic Anhydrase Ii (Hca Ii) (E.C.4....)	157	3e-37	
gi 442826 pdb 1DCA	Carbonic Anhydrase II (Carbonate Dehyd...	157	3e-37	
gi 1065012 pdb 1CNJ	Carbonic Anhydrase Ii (Carbonate Dehy...	157	3e-37	
gi 1345651 sp P48282 CAH1_SHEEP	Carbonic anhydrase I (Carbo...	157	3e-37	
gi 229981 pdb 1HED	Carbonic Anhydrase II (Carbonate Dehyd...	157	3e-37	
gi 442703 pdb 1CAL	Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu...	157	3e-37	
gi 229657 pdb 12CA	Carbonic Anhydrase II (Carbonate Dehyd...	157	3e-37	
gi 1065011 pdb 1CNI	Carbonic Anhydrase Ii (Carbonate Dehy...	157	3e-37	
gi 999932 pdb 1CCS	Carbonic Anhydrase Ii (Carbonate Dehyd...	157	4e-37	
gi 1065001 pdb 1CNG	Carbonic Anhydrase Ii (Carbonate Dehy...	157	4e-37	
gi 442700 pdb 1CAT	Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu...	157	4e-37	
gi 229978 pdb 1HEA	Carbonic Anhydrase II (Carbonate Dehyd...	157	4e-37	
gi 999632 pdb 1YDD	Carbonic Anhydrase Ii (Carbonate Dehyd...	157	4e-37	
gi 2554664 pdb 1H9N	H119n Carbonic Anhydrase Ii	157	4e-37	
gi 2554643 pdb 2H4N	H94n Carbonic Anhydrase Ii Complexed ...	157	4e-37	
gi 24987658 pdb 1LZV A	Chain A, Site-Specific Mutant (Tyr7 ...)	157	4e-37	
gi 231320 pdb 9CA2	Carbonic Anhydrase II (Carbonate Dehyd...	157	4e-37	
gi 1168741 sp P00919 CAH2_RABIT	Carbonic anhydrase II (Carb...	157	5e-37	
gi 999935 pdb 1CCT	Carbonic Anhydrase Ii (Carbonate Dehyd...	156	5e-37	
gi 1289219 emb CAA29417.1	carbonic anhydrase II [Gallus ga...	156	5e-37	

## Alignments

Get selected sequences

Select all

Deselect all

>gi|6912284|ref|NP\_036245.1| carbonic anhydrase XIV precursor; carbonic dehydratase [Homo sapiens]

gi|8928036|sp|Q9ULX7|CAHE\_HUMAN Carbonic anhydrase XIV precursor (Carbonate dehydratase XIV (CA-XIV) (UNQ690/PRO1335)

gi|6009640|dbj|BAA85002.1| carbonic anhydrase 14 [Homo sapiens]

gi|21706779|gb|AAH34412.1| Carbonic anhydrase XIV, precursor [Homo sapiens]

gi|37182500|gb|AAQ89052.1| CA14 [Homo sapiens]

Length = 337

Score = 682 bits (1760), Expect = 0.0

Identities = 337/337 (100%), Positives = 337/337 (100%)

Query: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60  
 Sbjct: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120  
 Sbjct: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120

Query: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180  
 Sbjct: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240  
 Sbjct: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTLLFSTEEEPSKLLVQNYRALQPLNQRMFASFQAGSSYTTGEMLSLGVGILVG 300  
 Sbjct: 241 LEKLQGTLLFSTEEEPSKLLVQNYRALQPLNQRMFASFQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337  
 Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337

>gi|22760422|dbj|BAC11191.1| unnamed protein product [Homo sapiens]  
 Length = 337

Score = 681 bits (1756), Expect = 0.0

Identities = 336/337 (99%), Positives = 336/337 (99%)

Query: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60  
 Sbjct: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120  
 Sbjct: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120

Query: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180  
 Sbjct: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240  
 Sbjct: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTLLFSTEEEPSKLLVQNYRALQPLNQRMFASFQAGSSYTTGEMLSLGVGILVG 300  
 Sbjct: 241 LEKLQGTLLFSTEEEPSKLLVQNYRALQPLNQRMFASFQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337  
 Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337

>gi|6753264|ref|NP\_035927.1| carbonic anhydrase 14; CA XIV [Mus musculus]  
 gi|8928038|sp|Q9WVT6|CAHE\_MOUSE Carbonic anhydrase XIV precursor (Carbonate dehydratase XIV (CA-XIV))  
 gi|5030908|dbj|BAA78709.1| CA XIV [Mus musculus]  
 gi|28422260|gb|AAH46995.1| Carbonic anhydrase 14 [Mus musculus]  
 Length = 337

Score = 548 bits (1413), Expect = e-155  
 Identities = 283/337 (83%), Positives = 306/337 (90%)

Query: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60  
 MLF ALLL+V WILAADGG HWTYEGPHGQDHP SYPECG +AQSPI+IQTDSV FDPD  
 Sbjct: 1 MLFFALLLKVTWILAADGGHHWTYEGPHGQDHWPTSYPECGDAQSPINIQTDSVIFDPD 60

Query: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120  
 LPA+QPHGYDQ GTEPLDLHNNGHTVQLSLP TL+LGGLPRKY AAQLHLHWGQ+GS G  
 Sbjct: 61 LPAVQPHGYDQLGTEPLDLHNNGHTVQLSLPPTLHLGGLPRKYTAAQLHLHWGQGRGSLEG 120

Query: 121 SEHQINSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180  
 SEHQINSEAT AELH+VHYDS SY SLSEAA++PQGLAVLGILIEVGET+N AY+HILS  
 Sbjct: 121 SEHQINSEATAAELHVHYDSQSYSSLSEAAQKPQGLAVLGILIEVGETENPAYDHILSR 180

Query: 181 LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240  
 LHE+R+KDQKTSVPPF++REL P+QL Q+FRYNGSLTTPPCYQSVLWTVF RR+QISM Q  
 Sbjct: 181 LHEIRYKDQKTSVPPFSVRELFPQLEQFFRYNGSLTTPPCYQSVLWTVFNRAQISMGG 240

Query: 241 LEKLQGTLFSTEEPSKLLVQNYRALQPLNQRMFASFQAGSSYTTGEMLSLGVGILVG 300  
 LEKLQ TL STEE+PS+ LVQNYR QPLNQR +FASFQAG YTTGEML LGVGIL G  
 Sbjct: 241 LEKLQETLSSTEEDPSEPLVQNYRVPQPLNQRRTIFASFQAGPLYTTGEMLGLGVGILAG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337  
 CLCLLLAVYFIA+KIRKKRL NRKSVVFTSA+ATTEA  
 Sbjct: 301 CLCLLLAVYFIAQKIRKKRLGNRKSVVFTSARATTEA 337

>gi|47168790|pdb|1RJ5|A Chain A, Crystal Structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv  
 gi|47168791|pdb|1RJ5|B Chain B, Crystal Structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv  
 gi|47168792|pdb|1RJ6|A Chain A, Crystal Structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv In Complex With Acetazolamide  
 gi|47168793|pdb|1RJ6|B Chain B, Crystal Structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv In Complex With Acetazolamide  
 Length = 261

Score = 438 bits (1127), Expect = e-122  
 Identities = 216/261 (82%), Positives = 236/261 (90%)

Query: 18 GGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPL 77  
 GG HWTYEGPHGQDHP SYPECG +AQSPI+IQTDSV FDPDLP+QPHGYDQ GTEPL  
 Sbjct: 1 GGHHWTYEGPHGQDHWPTSYPECGDAQSPINIQTDSVIFDPDLP+QPHGYDQLGTEPL 60

Query: 78 DLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEATFAELHIV 137  
 DLHNNGHTVQLSLP TL+LGGLPRKY AAQLHLHWGQ+GS GSEH INSEAT AELH+V  
 Sbjct: 61 DLHNNGHTVQLSLPPTLHLGGLPRKYTAAQLHLHWGQGRGSLEGSEHHINSEATAAELHV 120

Query: 138 HYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFN 197  
 HYDS SY SLSEAA++PQGLAVLGILIEVGET+N AY+HILS LHE+R+KDQKTSVPPF+  
 Sbjct: 121 HYDSQSYSSLSEAAQKPQGLAVLGILIEVGETENPAYDHILSR LHEIRYKDQKTSVPPFS 180

Query: 198 LRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEPSK 257  
 +REL P+QL Q+FRYNGSLTTPPCYQSVLWTVF RR+QISM QLEKLQ TL STEE+PS+  
 Sbjct: 181 VRELFPQLEQFFRYNGSLTTPPCYQSVLWTVFNRAQISMGGLEKLQETLSSTEEDPSE 240

Query: 258 LLVQNYRALQPLNQRMFASF 278  
 LVQNYR QPLNQR +FASF  
 Sbjct: 241 PLVQNYRVPQPLNQRRTIFASF 261

Sequences producing significant alignments:			Score (bits)	E Value	
gi 37182499 gb AY358689.1	Homo sapiens clone DNA62812 CA14...	3366	0.0	LU	
gi 6912283 ref NM_012113.1	Homo sapiens carbonic anhydrase...	3350	0.0	LUG	
gi 6009639 dbj AB025904.1	Homo sapiens mRNA for carbonic a...	3350	0.0	LUG	
gi 22760421 dbj AK074765.1	Homo sapiens cDNA FLJ90284 fis,...	3313	0.0	LU	
gi 21706778 gb BC034412.1	Homo sapiens carbonic anhydrase ...	3299	0.0	LUG	
gi 19309420 emb AL138795.21	Human DNA sequence from clone ...	948	0.0		
gi 28422259 gb BC046995.1	Mus musculus carbonic anhydrase ...	805	0.0	LU	
gi 6753263 ref NM_011797.1	Mus musculus carbonic anhydrase...	805	0.0	LUG	
gi 5030907 dbj AB005450.1	Mus musculus mRNA for CA XIV, co...	805	0.0	LUG	
gi 15384634 emb AL451074.13	Human DNA sequence from clone ...	650	0.0	L	
gi 12848980 dbj AK012316.1	Mus musculus 11 days embryo who...	454	e-124	LUG	
gi 34858062 ref XM_342297.1	Rattus norvegicus similar to C...	373	e-100	LU	
gi 15082388 gb BC012108.1	Homo sapiens cDNA clone MGC:2010...	287	4e-74	LUG	
gi 26801277 gb AC092855.39	Mus musculus chromosome 3 clone...	184	4e-43		
gi 26084135 dbj AK034693.1	Mus musculus 12 days embryo emb...	167	1e-37	U	
gi 12844826 dbj AK009805.1	Mus musculus adult male tongue ...	86	3e-13	LUG	
gi 33569140 emb AL845336.9	Mouse DNA sequence from clone R...	74	1e-09		
gi 23334838 gb AC123032.5	Mus musculus BAC clone RP24-480K...	72	4e-09		
gi 46518694 gb AC125192.3	Mus musculus BAC clone RP23-266B...	72	4e-09		
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gi 21955088 gb AC122003.2	Mus musculus BAC clone RP24-336G...	68	7e-08		
gi 3252819 gb AC004382.1	HUAC004382 Homo sapiens Chromosome...	68	7e-08	LUG	
gi 45476650 gb AC122746.7	Mus musculus chromosome 17, clon...	68	7e-08		
gi 4508108 gb AC005101.2	Homo sapiens BAC clone CTA-352J5 ...	68	7e-08	L	
gi 50355915 gb AC124516.4	Mus musculus chromosome 12 clone...	66	3e-07		
gi 50199072 gb AC110559.11	Mus musculus chromosome 7, clon...	66	3e-07		
gi 25046688 gb AC112147.5	Mus musculus BAC clone RP23-175E...	66	3e-07		
gi 37620322 gb AC111047.9	Mus musculus chromosome 3, clone...	66	3e-07		
gi 33590044 gb AC118614.12	Mus musculus chromosome 18, clo...	66	3e-07		
gi 29501916 gb AC099600.5	Mus musculus chromosome 15, clon...	66	3e-07		
gi 33342291 gb AC126722.7	Rattus norvegicus 4 BAC CH230-5L...	66	3e-07		
gi 42475822 emb AL928891.20	Mouse DNA sequence from clone ...	66	3e-07		
gi 47131369 gb AC147160.2	Mus musculus BAC clone RP24-336A...	66	3e-07		
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## Alignments

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Score = 3366 bits (1698), Expect = 0.0  
Identities = 1701/1701 (100%)  
Strand = Plus / Plus

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Identities = 1698/1701 (99%)  
Strand = Plus / Plus

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Score = 3350 bits (1690), Expect = 0.0

Identities = 1698/1701 (99%)

Strand = Plus / Plus

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Query: 301 atttggatcctggctgcagatgggggtcaacactggacgtatgagggccacatggtcag 360  
Sbjct: 340 atttggatcctggctgcagatgggggtcaacactggacgtatgagggccacatggtcag 399

Query: 361 gaccattggccagcctcttaccctgagtggtggaacaatgccagtcgcccacatcgatatt 420  
Sbjct: 400 gaccattggccagcctcttaccctgagtggtggaacaatgccagtcgcccacatcgatatt 459

Query: 421 cagacagacagtgtgacatttgaccctgatttgctgctctgcagccccacggatatgac 480  
Sbjct: 460 cagacagacagtgtgacatttgaccctgatttgctgctctgcagccccacggatatgac 519

Query: 481 cagcctggcaccgagcctttggacctgcacaacaatggccacacagtgaactctctctg 540  
Sbjct: 520 cagcctggcaccgagcctttggacctgcacaacaatggccacacagtgaactctctctg 579

Query: 541 ccctctaccctgtatctgggtggacttccccgaaaatatgtagctgccagctccacctg 600  
Sbjct: 580 ccctctaccctgtatctgggtggacttccccgaaaatatgtagctgccagctccacctg 639

Query: 601 cactggggtcagaaaggatccccaggggggtcagaacaccagatcaacagtgaagccaca 660  
Sbjct: 640 cactggggtcagaaaggatccccaggggggtcagaacaccagatcaacagtgaagccaca 699

Query: 661 tttgcagagctccacattgtacattatgactctgattcctatgacagcttgagtgggct 720  
Sbjct: 700 tttgcagagctccacattgtacattatgactctgattcctatgacagcttgagtgggct 759

Query: 721 gctgagaggcctcagggcctggctgtcctgggcatcctaattgaggtgggtgagactaag 780  
Sbjct: 760 gctgagaggcctcagggcctggctgtcctgggcatcctaattgaggtgggtgagactaag 819

Query: 781 aatatagcttatgaacacattctgagtcacttgcatgaagtcaggcataaagatcagaag 840  
Sbjct: 820 aatatagcttatgaacacattctgagtcacttgcatgaagtcaggcataaagatcagaag 879

Query: 841 acctcagtgccctcccttcaacctaaagagagctgctccccaacagctggggcagttctc 900

Sbjct: 880 |||||  
acctcagtcctcccttcaacctaagagagctgctccccaacagctggggcagtacttc 939

---

Query: 901 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 960  
Sbjct: 940 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 999

Query: 961 tatagaaggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1020  
Sbjct: 1000 tatagaaggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1059

Query: 1021 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1080  
Sbjct: 1060 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1119

Query: 1081 cagcgcatggtctttgcttctttcatccaagcaggatcctcgataccacaggtgaaatg 1140  
Sbjct: 1120 cagcgcatggtctttgcttctttcatccaagcaggatcctcgataccacaggtgaaatg 1179

Query: 1141 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1200  
Sbjct: 1180 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1239

Query: 1201 attgctagaaagattcggagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1260  
Sbjct: 1240 attgctagaaagattcggagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1299

Query: 1261 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1320  
Sbjct: 1300 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1359

Query: 1321 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1380  
Sbjct: 1360 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1419

Query: 1381 gagtagtaagcagatgtcctccttccctggacatctcttagagaggaatggaccaggc 1440  
Sbjct: 1420 gagtagtaagcagatgtcctccttccctggacatctcttagagaggaatggaccaggc 1479


Query: 1441 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1500  
Sbjct: 1480 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1539

Query: 1501 gaaatcgctgtgttggttaatgcagagancaaactctgttttagttgcaggggaagtttggg 1560  
Sbjct: 1540 gaaatcgctgtgttggttaatgcagagaacaaactctgttttagttgcaggggaagtttggg 1599

Query: 1561 atatacccccagtcctctacccccctcacttttatggccctttccctagatatatactgcgg 1620  
Sbjct: 1600 atatacccccagtcctctacccccctcacttttatggccctttccctagatatatactgcgg 1659

Query: 1621 gatctctccttaggataaagagttgctgttggaagttgtatattttgatcaatatatttg 1680  
Sbjct: 1660 gatctctccttaggataaagagttgctgttggaagttgtatattttgatcaatatatttg 1719

Query: 1681 gaaattaaagtttctgacttt 1701  
Sbjct: 1720 gaaattaaagtttctgacttt 1740

>gi|22760421|dbj|AK074765.1|  Homo sapiens cDNA FLJ90284 fis, clone NT2RP1000613, weakly si  
CARBONIC ANHYDRASE VI (EC 4.2.1.1)  
Length = 1771

Score = 3313 bits (1671), Expect = 0.0  
Identities = 1682/1686 (99%)  
Strand = Plus / Plus

```
Query: 1   gagactgcagagggagataaaagagagagggcaaagaggcagcaagagatttgtcctgggg 60
Sbjct: 86   gagactgcagagggagataaaagagagagggcaaagaggcagcaagagatttgtcctgggg 145

Query: 61   atccagaaacccatgataccctactgaacaccgaatcccctggaagcccacagagacaga 120
Sbjct: 146  atccagaaacccatgataccctactgaacaccgaatcccctggaagcccacagagacaga 205

Query: 121  gacagcaagagaagcagagataaatacactcacgccaggagctcgctcgctctctctctc 180
Sbjct: 206  gacagcaagagaagcagagataaatacactcacgccaggagctcgctcgctctctctctc 265

Query: 181  tctctctcactcctccctccctctctctctgctgtcctagtcctctagtcctcaaattc 240
Sbjct: 266  tctctctcactcctccctccctctctctctgctgtcctagtcctctagtcctcaaattc 325

Query: 241  ccagtcccctgcaccccttcctgggacactatgttgttctccgccctcctgctggagggtg 300
Sbjct: 326  ccagtcccctgcaccccttcctgggacactatgttgttctccgccctcctgctggagggtg 385

Query: 301  atttggatcctggctgcagatgggggtcaacactggacgtatgagggccacatggtcag 360
Sbjct: 386  atttggatcctggctgcagatgggggtcaacactggacgtatgagggccacatggtcag 445

Query: 361  gaccattggccagcctcttaccctgagtgtggaacaatgccagtcgcccacatcgatatt 420
Sbjct: 446  gaccattggccagcctcttaccctgagtgtggaacaatgccagtcgcccacatcgatatt 505

Query: 421  cagacagacagtgtgacatttgaccctgatttgctgctctgcagccccacggatatgac 480
Sbjct: 506  cagacagacagtgtgacatttgaccctgatttgctgctctgcagccccacggatatgac 565

Query: 481  cagcctggcaccgagccttggacctgcacaacaatggccacacagtgaactctctctg 540
Sbjct: 566  cagcctggcaccgagccttggacctgcacaacaatggccacacagtgaactctctctg 625

Query: 541  ccctctaccctgtatctgggtggacttccccgaaaatatgtagctgccagctccacctg 600
Sbjct: 626  ccctctaccctgtatctgggtggacttccccgaaaatatgtagctgccagctccacctg 685

Query: 601  cactgggggtcagaaaggatccccaggggggtcagaacaccagatcaacagtgaagccaca 660
Sbjct: 686  cactgggggtcagaaaggatccccaggtgggtcagaacaccagatcaacagtgaagccaca 745

Query: 661  tttgcagagctccacattgtacattatgactctgattcctatgacagcttgagtgaggct 720
Sbjct: 746  tttgcagagctccacattgtacattatgactctgattcctatgacagcttgagtgaggct 805
```

Query: 721 gctgagaggcctcagggcctggctgtcctgggcatcctaattgaggtgggtgagactaag 780

Sbjct: 806 gctgagaggcctcagggcctggctgtcctgggcatcctaattgaggtgggtgagactaag 865

Query: 781 aatatagcttatgaacacattctgagtcacttgcatgaagtcaggcataaagatcagaag 840

Sbjct: 866 aatatagcttatgaacacattctgagtcacttgcatgaagtcaggcataaagatcagaag 925

Query: 841 acctcagtgccctcccttcaacctaagagagctgctccccaacagctggggcagttacttc 900

Sbjct: 926 acctcagtgccctcccttcaacctaagagagctgctccccaacagctggggcagttacttc 985

Query: 901 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 960

Sbjct: 986 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 1045

Query: 961 tatagaagggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1020

Sbjct: 1046 tatagaagggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1105

Query: 1021 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1080

Sbjct: 1106 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1165

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Sbjct: 1166 cagcgcatgggtctttgcttctttcatccaagcaggatcctcgataaccacaggtgaaatg 1225

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Sbjct: 1226 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1285

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Sbjct: 1286 attgctagaaagattcggagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1345

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Sbjct: 1466 gagtagtaagcagatgtcctccttccccctggacatctcttagagaggaatggaccaggc 1525

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Sbjct: 1526 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1585

Query: 1501 gaaatcgctgtgttggttaatgcagagancaaactctgtttagttgcaggggaagtttggg 1560

Sbjct: 1586 gaaatcgctgtgttggttaatgcagagaacaaactctgtttagttgcaggggaagtttggg 1645

Query: 1561 atataccccaagtcctctacccccctcacttttatggccctttccctagatatactgcgg 1620

Sbjct: 1646 atatacccccagtcctctacccccctcacttttatggccctttccctagatataactgcgg 1705

Query: 1621 gatctctccttaggataaaagagttgctgttgaagttgtatattttgatcaatatatttg 1680

Sbjct: 1706 gatctctccttaggataaaagagttgctgttgaagttgtatattttgatcaatatatttg 1765

Query: 1681 gaaatt 1686

Sbjct: 1766 gaaatt 1771

>gi|21706778|gb|BC034412.1| **LOC** Homo sapiens carbonic anhydrase XIV, mRNA (cDNA clone MGC:34  
IMAGE:5175251), complete cds  
Length = 1767

Score = 3299 bits (1664), Expect = 0.0

Identities = 1669/1671 (99%)

Strand = Plus / Plus

Query: 31 caaagaggcagcaagagatttgcctggggatccagaaacccatgataccctactgaaca 90

Sbjct: 1 caaagaggcagcaagagatttgcctggggatccagaaacccatgataccctactgaaca 60

Query: 91 ccgaatcccctggaagcccacagagacagagacagcaagagaagcagagataaaatacact 150

Sbjct: 61 ccgaatcccctggaagcccacagagacagagacagcaagagaagcagagataaaatacact 120

Query: 151 cacgccaggagctcgctcgctctctctctctctctcactcctccctccctctctctct 210

Sbjct: 121 cacgccaggagctcgctcgctctctctctctctctcactcctccctccctctctctct 180

Query: 211 gcctgtccttagtcctctagtcctcaaattcccagtcctcctgcaccccttcctgggacact 270

Sbjct: 181 gcctgtccttagtcctctagtcctcaaattcccagtcctcctgcaccccttcctgggacact 240

Query: 271 atgttggttctccgccctcctgctggaggtgatttggatcctggctgcagatgggggtcaa 330

Sbjct: 241 atgttggttctccgccctcctgctggaggtgatttggatcctggctgcagatgggggtcaa 300

Query: 331 cactggacgtatgagggcccacatggtcaggaccattggccagcctcttaccctgagtgt 390

Sbjct: 301 cactggacgtatgagggcccacatggtcaggaccattggccagcctcttaccctgagtgt 360

Query: 391 ggaacaatgcccagtcgcccacatcgatattcagacagacagtgtagacatttgaccctgat 450

Sbjct: 361 ggaacaatgcccagtcgcccacatcgatattcagacagacagtgtagacatttgaccctgat 420

Query: 451 ttgcctgctctgcagccccacggatatgaccagcctggcaccgagccttggacctgcac 510

Sbjct: 421 ttgcctgctctgcagccccacggatatgaccagcctggcaccgagccttggacctgcac 480

Query: 511 aacaatggccacacagtgcgaactctctctgccctctaccctgtatctgggtggacttccc 570

Sbjct: 481 aacaatggccacacagtgcgaactctctctgccctctaccctgtatctgggtggacttccc 540

Query: 571 cgaaaaatatgtagctgcccagctccacctgcactggggtcagaaaggatccccagggggg 630

Sbjct: 541 cgaaaaatatgtagctgcccagctccacctgcactggggtcagaaaggatccccagggggg 600

Query: 631 tcagaacaccagatcaacagtgaagccacatttgagagctccacattgtacattatgac 690  
Sbjct: 601 tcagaacaccagatcaacagtgaagccacatttgagagctccacattgtacattatgac 660

Query: 691 tctgattcctatgacagcttgagtgaggctgctgagaggcctcagggcctggctgtcctg 750  
Sbjct: 661 tctgattcctatgacagcttgagtgaggctgctgagaggcctcagggcctggctgtcctg 720

Query: 751 ggcatcctaattgaggtgggtgagactaagaatatagcttatgaacacattctgagtcac 810  
Sbjct: 721 ggcatcctaattgaggtgggtgagactaagaatatagcttatgaacacattctgagtcac 780

Query: 811 ttgcatgaagtcaggcataaagatcagaagacctcagtgccctcccttaacctaagagag 870  
Sbjct: 781 ttgcatgaagtcaggcataaagatcagaagacctcagtgccctcccttaacctaagagag 840

Query: 871 ctgctccccaacagctggggcagttacttccgctacaatggctcgtcacaactccccct 930  
Sbjct: 841 ctgctccccaacagctggggcagttacttccgctacaatggctcgtcacaactccccct 900

Query: 931 tgctaccagagtgtgctctggacagttttttatagaaggctccagatttcaatggaacag 990  
Sbjct: 901 tgctaccagagtgtgctctggacagttttttatagaaggctccagatttcaatggaacag 960

Query: 991 ctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctggta 1050  
Sbjct: 961 ctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctggta 1020

Query: 1051 cagaactaccgagcccttcagcctctcaatcagcgcatggctcttgcttcttcatccaa 1110  
Sbjct: 1021 cagaactaccgagcccttcagcctctcaatcagcgcatggctcttgcttcttcatccaa 1080

Query: 1111 gcaggatcctcgataaccacaggtgaaatgctgagtctaggtgtaggaatcttggttggc 1170  
Sbjct: 1081 gcaggatcctcgataaccacaggtgaaatgctgagtctaggtgtaggaatcttggttggc 1140

Query: 1171 tgtctctgccttctcctggctgtttatttcattgctagaaagattcggagaagaggctg 1230  
Sbjct: 1141 tgtctctgccttctcctggctgtttatttcattgctagaaagattcggagaagaggctg 1200

Query: 1231 gaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactgaggcataaattcct 1290  
Sbjct: 1201 gaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactgaggcataaattcct 1260

Query: 1291 tctcagataccatggatgtggatgacttcccttcatgcctatcaggaagcctctaaaatg 1350  
Sbjct: 1261 tctcagataccatggatgtggatgacttcccttcatgcctatcaggaagcctctaaaatg 1320

Query: 1351 ggggtgtaggatctggccagaaacactgtaggagtagtaagcagatgtcctccttcccctg 1410  
Sbjct: 1321 ggggtgtaggatctggccagaaacactgtaggagtagtaagcagatgtcctccttcccctg 1380

Query: 1411 gacatctcttagagaggaatggaccaggctgtcattccaggaagaactgcagagccttc 1470  
Sbjct: 1381 gacatctccttagagaggaatggaccaggctgtcattccaggaagaactgcagagccttc 1440

Query: 1471 agcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttggttaatgcagaganca 1530



|||||  
Sbjct: 1441 agcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttattaatgcagagaaca 1500

Query: 1531 aactctgtttagttgcaggggaagtttgggatataaccccaaagtcctctaccccctcact 1590  
|||||

Sbjct: 1501 aactctgtttagttgcaggggaagtttgggatataaccccaaagtcctctaccccctcact 1560

Query: 1591 tttatggccctttccctagatatactgcgggatctctccttaggataaagagttgctgtt 1650  
|||||

Sbjct: 1561 tttatggccctttccctagatatactgcgggatctctccttaggataaagagttgctgtt 1620

Query: 1651 gaagttgtatatattttgatcaatatatttggaaattaaagtttctgacttt 1701  
|||||

Sbjct: 1621 gaagttgtatatattttgatcaatatatttggaaattaaagtttctgacttt 1671

>gi|19309420|emb|AL138795.21| Human DNA sequence from clone RP4-790G17 on chromosome 1q21.1-  
complete sequence  
Length = 132823

Score = 948 bits (478), Expect = 0.0

Identities = 483/485 (99%)

Strand = Plus / Plus

Query: 1217 ggaagaagaggctggaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactg 1276  
|||||

Sbjct: 78784 ggaagaagaggctggaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactg 78843

Query: 1277 aggcataaattccttctcagataccatggatgtggatgacttccttcatgcctatcagg 1336  
|||||

Sbjct: 78844 aggcataaattccttctcagataccatggatgtggatgacttccttcatgcctatcagg 78903

Query: 1337 aagcctctaaaatgggggtgtaggatctggccagaaacactgtaggagtagtaagcagatg 1396  
|||||

Sbjct: 78904 aagcctctaaaatgggggtgtaggatctggccagaaacactgtaggagtagtaagcagatg 78963

Query: 1397 tcctccttcccctggacatctcttagagaggaatggaccaggctgtcattccaggaaga 1456  
|||||

Sbjct: 78964 tcctccttcccctggacatctcttagagaggaatggaccaggctgtcattccaggaaga 79023

Query: 1457 actgcagagccttcagcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttgt 1516  
|||||

Sbjct: 79024 actgcagagccttcagcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttgt 79083

Query: 1517 taatgcagagancaaactctgttttagttgcaggggaagtttgggatataaccccaaagtcc 1576  
|||||

Sbjct: 79084 taatgcagagaacaaactctgttttagttgcaggggaagtttgggatataaccccaaagtcc 79143

Query: 1577 tctaccccctcacttttatggccctttccctagatatactgcgggatctctccttaggat 1636  
|||||

Sbjct: 79144 tctaccccctcacttttatggccctttccctagatatactgcgggatctctccttaggat 79203

Query: 1637 aaagagttgctgttgaagttgtatatattttgatcaatatatttggaaattaaagtttctg 1696  
|||||

Sbjct: 79204 aaagagttgctgttgaagttgtatatattttgatcaatatatttggaaattaaagtttctg 79263

Query: 1697 acttt 1701  
|||||

Sbjct: 79264 acttt 79268





Score = 176 bits (89), Expect = 1e-40

Identities = 89/89 (100%)

Strand = Plus / Plus

Query: 1130 cagggtgaaatgctgagcttaggtgtaggaatcttggttggtgctgtctctgccttctcctgg 1189  
|||||  
Sbjct: 77982 cagggtgaaatgctgagcttaggtgtaggaatcttggttggtgctgtctctgccttctcctgg 78041

Query: 1190 ctgtttatttcattgctagaaagattcgg 1218  
|||||  
Sbjct: 78042 ctgtttatttcattgctagaaagattcgg 78070

Score = 137 bits (69), Expect = 9e-29

Identities = 69/69 (100%)

Strand = Plus / Plus

Query: 764 aggtgggtgagactaagaatatagcttatgaacacattctgagtcacttgcatagaagtca 823  
|||||  
Sbjct: 76993 aggtgggtgagactaagaatatagcttatgaacacattctgagtcacttgcatagaagtca 77052

Query: 824 ggcataaag 832  
|||||  
Sbjct: 77053 ggcataaag 77061

Score = 50.1 bits (25), Expect = 0.016

Identities = 25/25 (100%)

Strand = Plus / Plus


Query: 1110 agcaggatcctcgtataccacaggt 1134  
|||||  
Sbjct: 77848 agcaggatcctcgtataccacaggt 77872

Score = 46.1 bits (23), Expect = 0.25

Identities = 23/23 (100%)

Strand = Plus / Plus

Query: 325 ggtcaacactggacgtatgaggg 347  
|||||  
Sbjct: 74337 ggtcaacactggacgtatgaggg 74359

>[gi|28422259|gb|BC046995.1](#)  Mus musculus carbonic anhydrase 14, mRNA (cDNA clone MGC:54680 IMAGE:6491779), complete cds  
Length = 1654

Score = 805 bits (406), Expect = 0.0

Identities = 844/990 (85%)

Strand = Plus / Plus

Query: 270 tatgttggttctccgccctcctgctggaggtgatttggatcctggctgcagatgggggtca 329  
|||||  
Sbjct: 247 tatgttggttcttctcgtctcctgttaaagggtgacttggatcctggctgcagatgggggtca 306

Query: 330 aactggacgtatgagggccacatgggtcaggaccattggccagcctcttaccctgagtg 389  
|||||  
Sbjct: 307 ccactggacatatgaaggccacacgggtcaggaccattggccaacctcttatcctgagtg 366

7/26/04



Query: 990 gctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctggt 1049

Sbjct: 985 gttagagaagctccaggagacattgtcctctacagaagaggacccctctgagcccttgt 1044

Query: 1050 acagaactaccgagcccttcagcctctcaatcagcgcatggctctttgcttctttcatcca 1109

Sbjct: 1045 acagaactacagagtccccagcctctcaaccagaggaccatctttgcttctttcatcca 1104

Query: 1110 agcaggatcctcgtataccacagggtgaaatgctgagtctaggtgtaggaatcttggttgg 1169

Sbjct: 1105 agcaggaccactgtataccacaggagagatgctgggtctaggtgtgggaatcttggttgg 1164

Query: 1170 ctgtctctgccttctcctggctgtttatttcattgctagaaagattcggaagaagaggct 1229

Sbjct: 1165 atgtctttgccttctgctggctgtttatttcattgctcaaaaaattaggaagaagcggct 1224

Query: 1230 ggaaaaccgaaagagtgtggtcttcacctc 1259

Sbjct: 1225 gggaaacaggaaaagtgtggttttcacctc 1254

>gi|5030907|dbj|AB005450.1| **ELC** Mus musculus mRNA for CA XIV, complete cds  
Length = 1624

Score = 805 bits (406), Expect = 0.0

Identities = 844/990 (85%)

Strand = Plus / Plus

Query: 270 tatgttgttctccgccctcctgctggaggtgatttgatcctggctgcagatgggggtca 329

Sbjct: 265 tatgttgttcttctcgtctcctgttaaagggtgacttgatcctggctgcagatgggggtca 324

Query: 330 acactggacgtatgagggccacatgggtcaggaccattggccagcctcttaccctgagtg 389

Sbjct: 325 ccactggacatatgaaggccacacgggtcaggaccattggccaacctcttatcctgagtg 384

Query: 390 tggaaacaatgccagtcgcccacgatattcagacagacagtgtgacatttgaccctga 449

Sbjct: 385 tggaggcgatgccagtcgcccatcaatatccagacagacagtgtgatatttgacccga 444

Query: 450 tttgcctgctctgcagccccacggatatgaccagcctggcaccgagcctttggacctgca 509

Sbjct: 445 tctgcctgctgtacagccccatggatatgaccagcctgggactgagcctttggatctaca 504

Query: 510 caacaatggccacacagtgcactctctctgcccctctaccctgtatctgggtggacttcc 569

Sbjct: 505 caataatggccatacagtgcagctttccctgcccccaaccctgcacctgggtggactgcc 564

Query: 570 ccgaaaatatgtagctgccagctccacctgcactggggtcagaaaggatcccaggggg 629

Sbjct: 565 ccgaaaatacacagcagcccagctccacctgcactggggtcagagaggatccctcgaggg 624

Query: 630 gtcagaacaccagatcaacagtgaagccacatttgagagctccacattgtacattatga 689

Sbjct: 625 atcagagcaccagatcaacagtgaagccacggctgcggagctccacgtggttcactatga 684

Query: 690 ctctgattcctatgacagcttgagtgaggctgctgagaggcctcagggcctggctgtcct 749

Sbjct: 685 ctcccagtcctacagcagcttgagtgaggcagctcagaagccacagggcctggctgtcct 744

Query: 750 gggcatcctaattgaggtgggtgagactaagaatatagcttatgaacacattctgagtca 809

Sbjct: 745 aggcattcctcattgaggtgggcgagactgagaatccagcttatgatcacattctgagtcg 804

Query: 810 cttgcatgaagtcaggcataaagatcagaagacctcagtcctcccttcaacctaagaga 869

Sbjct: 805 tctacatgaaataagatacaaagatcagaagacctctgtgcctcccttcagcgtgagaga 864

Query: 870 gctgctccccaacagctggggcagttctccgctacaatggctcgctcacaactccccc 929

Sbjct: 865 gctgttccccaacagctggagcaattcttccgctacaacggctcactcacaactccccc 924

Query: 930 ttgctaccagagtgtgctctggacagtttttatagaagggtcccagatttcaatggaaca 989

Sbjct: 925 ctgctaccagagtgtgctctggacagtcttcaacagaagggccagatttcaatgggaca 984

Query: 990 gctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctggt 1049

Sbjct: 985 gttagagaagctccaggagacattgtcctctacagaagaggacccctctgagcccttgt 1044

Query: 1050 acagaactaccgagcccttcagcctctcaatcagcgcatggtctttgcttctttcatcca 1109

Sbjct: 1045 acagaactacagagtccccagcctctcaaccagaggaccatctttgcttctttcatcca 1104

Query: 1110 agcaggatcctcgtataccacaggtgaaatgctgagtcctaggtgtaggaatcttggttg 1169

Sbjct: 1105 agcaggaccactgtataccacaggagagatgctgggtctaggtgtgggaatcttggttg 1164

Query: 1170 ctgtctctgccttctcctggctgtttatttcatctgtagaaagattcggaagaaggct 1229

Sbjct: 1165 atgtctttgccttctgctggctgtttatttcatcgctcaaaaattaggaagaagcggct 1224

Query: 1230 ggaaaaccgaaagagtgtggtcttcacctc 1259

Sbjct: 1225 gggaaacaggaaaagtgtggttttcacctc 1254



>gi|6912284|ref|NP\_036245.1| carbonic anhydrase XIV precursor; carbonic dehydratase [Homo sapiens]

gi|8928036|sp|Q9ULX7|CAHE\_HUMAN Carbonic anhydrase XIV precursor (Carbonate dehydratase XIV (CA-XIV) (UNQ690/PRO1335)

gi|6009640|dbj|BAA85002.1| carbonic anhydrase 14 [Homo sapiens]

gi|21706779|gb|AAH34412.1| Carbonic anhydrase XIV, precursor [Homo sapiens]

gi|37182500|gb|AAQ89052.1| CA14 [Homo sapiens]

Length = 337

Score = 682 bits (1760), Expect = 0.0

Identities = 337/337 (100%), Positives = 337/337 (100%)

```

Query: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
          MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD
Sbjct: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61  LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120
          LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG
Sbjct: 61  LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120

Query: 121 SEHQINSEATFAELHIVHYSDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
          SEHQINSEATFAELHIVHYSDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH
Sbjct: 121 SEHQINSEATFAELHIVHYSDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
          LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ
Sbjct: 181 LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300
          LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG
Sbjct: 241 LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
          CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337

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>gi|22760422|dbj|BAC11191.1| unnamed protein product [Homo sapiens]

Length = 337

Score = 681 bits (1756), Expect = 0.0

Identities = 336/337 (99%), Positives = 336/337 (99%)

```

Query: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
          MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD
Sbjct: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61  LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120
          LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG
Sbjct: 61  LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120

Query: 121 SEHQINSEATFAELHIVHYSDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
          SEHQINSEATFAELHIVHYSDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH
Sbjct: 121 SEHQINSEATFAELHIVHYSDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
          LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ
Sbjct: 181 LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300
          LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG
Sbjct: 241 LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
          CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337

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      |||
Sbjct: 1000 tatagaagggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1059

Query: 1021 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagccttcaat 1080
      |||
Sbjct: 1060 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagccttcaat 1119

Query: 1081 cagcgcattggtctttgcttctttcatccaagcaggatcctcgtataccacaggtgaaatg 1140
      |||
Sbjct: 1120 cagcgcattggtctttgcttctttcatccaagcaggatcctcgtataccacaggtgaaatg 1179

Query: 1141 ctgagtctaggtgtaggaatcttggttggtgctgtctctgccttctcctggctgtttatttc 1200
      |||
Sbjct: 1180 ctgagtctaggtgtaggaatcttggttggtgctgtctctgccttctcctggctgtttatttc 1239

Query: 1201 attgctagaaagattcggagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1260
      |||
Sbjct: 1240 attgctagaaagattcggagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1299

Query: 1261 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1320
      |||
Sbjct: 1300 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1359

Query: 1321 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1380
      |||
Sbjct: 1360 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1419

Query: 1381 gagtagtaagcagatgtcctccttcccctggacatctcttagagaggaatggaccaggc 1440
      |||
Sbjct: 1420 gagtagtaagcagatgtcctccttcccctggacatctcttagagaggaatggaccaggc 1479

Query: 1441 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1500
      |||
Sbjct: 1480 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1539

Query: 1501 gaaatcgctgtgttggttaatgcagagancaaactctgttttagttgcaggggaagtttggg 1560
      |||
Sbjct: 1540 gaaatcgctgtgttggttaatgcagagaacaaactctgttttagttgcaggggaagtttggg 1599

Query: 1561 atataccccaaagtcctctaccccctcacttttatggccctttccctagatatactgcgg 1620
      |||
Sbjct: 1600 atataccccaaagtcctctaccccctcacttttatggccctttccctagatatactgcgg 1659

Query: 1621 gatctctccttaggataaagagttgctgttggaagttgtatatattttgatcaatatatttg 1680
      |||
Sbjct: 1660 gatctctccttaggataaagagttgctgttggaagttgtatatattttgatcaatatatttg 1719

Query: 1681 gaaattaaagtttctgacttt 1701
      |||
Sbjct: 1720 gaaattaaagtttctgacttt 1740

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>gi|6009639|dbj|AB025904.1| **LOC** Homo sapiens mRNA for carbonic anhydrase 14, complete cds  
Length = 1757

Score = 3350 bits (1690), Expect = 0.0  
Identities = 1698/1701 (99%)  
Strand = Plus / Plus

7/26/04

Sbjct: 880 |||||  
acctcagtgctcccttcaacctaagagagctgctccccaacagctggggcagtacttc 939

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Query: 901 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 960  
Sbjct: 940 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 999

Query: 961 tatagaaggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1020  
Sbjct: 1000 tatagaaggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1059

Query: 1021 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1080  
Sbjct: 1060 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1119

Query: 1081 cagcgcatggtctttgcttctttcatccaagcaggatcctcgatataccacaggtgaaatg 1140  
Sbjct: 1120 cagcgcatggtctttgcttctttcatccaagcaggatcctcgatataccacaggtgaaatg 1179

Query: 1141 ctgagtctaggtgtaggaatcttggttggtgctgtctctgccttctcctggctgtttatttc 1200  
Sbjct: 1180 ctgagtctaggtgtaggaatcttggttggtgctgtctctgccttctcctggctgtttatttc 1239

Query: 1201 attgctagaaagattcggaagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1260  
Sbjct: 1240 attgctagaaagattcggaagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1299

Query: 1261 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1320  
Sbjct: 1300 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1359

Query: 1321 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1380  
Sbjct: 1360 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1419

Query: 1381 gagtagtaagcagatgtcctccttcccctggacatctcttagagaggaatggaccaggc 1440  
Sbjct: 1420 gagtagtaagcagatgtcctccttcccctggacatctcttagagaggaatggaccaggc 1479

Query: 1441 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1500  
Sbjct: 1480 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1539

Query: 1501 gaaatcgctgtgttggttaatgcagagancaaactctgttttagttgcaggggaagtttggg 1560  
Sbjct: 1540 gaaatcgctgtgttggttaatgcagagaacaaactctgttttagttgcaggggaagtttggg 1599

Query: 1561 atataccccaagtcctctacccccctcacttttatggccctttccctagatatatactgcgg 1620  
Sbjct: 1600 atataccccaagtcctctacccccctcacttttatggccctttccctagatatatactgcgg 1659

Query: 1621 gatctctccttaggataaagagttgctgttggaagttgtatatttttgatcaatatatttg 1680  
Sbjct: 1660 gatctctccttaggataaagagttgctgttggaagttgtatatttttgatcaatatatttg 1719

Query: 1681 gaaattaaagtttctgacttt 1701  
Sbjct: 1720 gaaattaaagtttctgacttt 1740